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Sim

[Click here to view these alignments graphically with the LALNVIEW program \(mime-type *chemical/x-aln2*\).](#)

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Results of SIM with:

Sequence 1: GLCM_HUMAN, (536 residues)
Sequence 2: seq (497 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

100.0% identity in 497 residues overlap; Score: 2673.0; Gap frequency: 0.0%

```

GLCM_HUMAN      40  ARPCIPKSFYGYSSVVCVCNATYCDSDPPTFPALGTFSTRSRRMELSMGPIQANH
seq              1  ARPCIPKSFYGYSSVVCVCNATYCDSDPPTFPALGTFSTRSRRMELSMGPIQANH
*****

GLCM_HUMAN     100  TGTGLLLTLQPEQKFQVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEGIGYNIIR
seq             61  TGTGLLLTLQPEQKFQVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEGIGYNIIR
*****

GLCM_HUMAN     160  VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLASPWT
seq            121  VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLASPWT
*****

GLCM_HUMAN     220  SPTWLKTNGAVNGKSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL
seq            181  SPTWLKTNGAVNGKSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL
*****

GLCM_HUMAN     280  LSGYPFQCLGFTPEHQRDIFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPE
seq            241  LSGYPFQCLGFTPEHQRDIFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPE
*****

```

GLCM_HUMAN 340 AAKYVHGI AVHWYLD FLAPAKATLGETHRLFPNTMLFA SEACVGSKFWEQSVRLGSWDRG
 seq 301 AAKYVHGI AVHWYLD FLAPAKATLGETHRLFPNTMLFA SEACVGSKFWEQSVRLGSWDRG

GLCM_HUMAN 400 MQYSHSIIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL
 seq 361 MQYSHSIIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL

GLCM_HUMAN 460 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGS AVVVV LNRSSKDVPLTIKDPAVGFL
 seq 421 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGS AVVVV LNRSSKDVPLTIKDPAVGFL

GLCM_HUMAN 520 ETISPGYSIHTYLWHRQ
 seq 481 ETISPGYSIHTYLWHRQ

31.8% identity in 22 residues overlap; Score: 32.0; Gap frequency: 0.0%

GLCM_HUMAN 303 LGPTLANSTH HNVRL LMLDDQR
 seq 53 MGPIQANHTGTGL LLLTLQPEQK
 ** ** * * *

31.8% identity in 22 residues overlap; Score: 32.0; Gap frequency: 0.0%

GLCM_HUMAN 92 MGPIQANHTGTGL LLLTLQPEQK
 seq 264 LGPTLANSTH HNVRL LMLDDQR
 ** ** * * *

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0.0%

GLCM_HUMAN 451 YKQPMFYHLGHFSKF
 seq 26 FDPPTFPALGTFSRY
 * * ** **

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0.0%

GLCM_HUMAN 65 FDPPTFPALGTFSRY
 seq 412 YKQPMFYHLGHFSKF
 * * ** **

28.6% identity in 14 residues overlap; Score: 27.0; Gap frequency: 0.0%

GLCM_HUMAN 421 NLALNPEGGPNWVR
 seq 173 SLLASPWTSPTWLK